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RAW SEQUENCE LISTING   DATE: 09/18/2001
PATENT APPLICATION: US/09/940,921   TIME: 10:36:16

Input Set : C:\Crf3\Datahold\09543955
Output Set: N:\CRF3\09182001\I940921.raw

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      4 <110> APPLICANT: Little, II, Roger G.
      6 <120> TITLE OF INVENTION: IDENTIFICAITON OF NOVEL ANTIMICROBIAL AGENTS USING
      7       METABOLIC OXIDATION-REDUCTION INDICATOR DYES
      9 <130> FILE REFERENCE: 27129/36226
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/940,921
C--> 12 <141> CURRENT FILING DATE: 2001-08-28
     14 <150> PRIOR APPLICATION NUMBER: 60/143,290
     15 <151> PRIOR FILING DATE: 1999-07-12
     17 <160> NUMBER OF SEQ ID NOS: 6
     19 <170> SOFTWARE: PatentIn Ver. 2.1
     21 <210> SEQ ID NO: 1
     22 <211> LENGTH: 1813
     23 <212> TYPE: DNA
     24 <213> ORGANISM: Homo sapiens
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     27 <221> NAME/KEY: CDS
     28 <222> LOCATION: (31)..(1491)
     30 <220> FEATURE:
     31 <221> NAME/KEY: mat_peptide
     32 <222> LOCATION: (124)..(1491)
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     35 caggccttga ggttttggca gctctggagg atg aga gag aac atg gcc agg ggc   54
     36                                     Met Arg Glu Asn Met Ala Arg Gly
     37                                     -30               -25
     39 cct tgc aac gcg ccg aga tgg gtg tcc ctg atg gtg ctc gtc gcc ata  102
     40 Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile
     41          -20             -15             -10
     43 ggc acc gcc gtg aca gcg gcc gtc aac cct ggc gtc gtg gtc agg atc  150
     44 Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile
     45          -5              -1  1               5
     47 tcc cag aag ggc ctg gac tac gcc agc cag cag ggg acg gcc gct ctg  198
     48 Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu
     49   10               15              20                      25
     51 cag aag gag ctg aag agg atc aag att cct gac tac tca gac agc ttt  246
     52 Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe
     53               30              35              40
     56 aag atc aag cat ctt ggg aag ggg cat tat agc ttc tac agc atg gac  294
     57 Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp
     58               45              50              55
     60 atc cgt gaa ttc cag ctt ccc agt tcc cag ata agc atg gtg ccc aat  342
     61 Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn
     62           60              65              70
     64 gtg ggc ctt aag ttc tcc atc agc aac gcc aat atc aag atc agc ggg  390
     65 Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly
     66       75              80              85
     68 aaa tgg aag gca caa aag aga ttc tta aaa atg agc ggc aat ttt gac  438
     69 Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp
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70  90                         95                        100                      105
72 ctg agc ata gaa ggc atg tcc att tcg gct gat ctg aag ctg ggc agt      486
73 Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser
74            110                     115            .           120
76 aac ccc acg tca ggc aag ccc acc atc acc tgc tcc agc tgc agc agc      534
77 Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser
78            125                     130                      135
80 cac atc aac agt gtc cac gtg cac atc tca aag agc aaa gtc ggg tgg      582
81 His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp
82            140                     145      .         150
84 ctg atc caa ctc ttc cac aaa aaa att gag tct gcg ctt cga aac aag      630
85 Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys
86     155                     160                  165
88 atg aac agc cag gtc tgc gag aaa gtg acc aat tct gta tcc tcc aag      678
89 Met Asn Ser Gln Val Cys Glu Lys Val Thr Asn Ser Val Ser Ser Lys
90 170                     175                  180                  185
92 ctg caa cct tat ttc cag act ctg cca gta atg acc aaa ata gat tct      726
93 Leu Gln Pro Tyr Phe Gln Thr Leu Pro Val Met Thr Lys Ile Asp Ser
94                190                     195         .      200
96 gtg gct gga atc aac tat ggt ctg gtg gca cct cca gca acc acg gct      774
97 Val Ala Gly Ile Asn Tyr Gly Leu Val Ala Pro Pro Ala Thr Thr Ala
98            205                     210                  215
100 gag acc ctg gat gta cag atg aag ggg gag ttt tac agt gag aac cac     822
101 Glu Thr Leu Asp Val Gln Met Lys Gly Glu Phe Tyr Ser Glu Asn His
102         220                     225                  230
104 cac aat cca cct ccc ttt gct cca cca gtg atg gag ttt ccc gct gcc     870
105 His Asn Pro Pro Pro Phe Ala Pro Pro Val Met Glu Phe Pro Ala Ala
106     235                     240                  245
108 cat gac cgc atg gta tac ctg ggc ctc tca gac tac ttc ttc aac aca     918
109 His Asp Arg Met Val Tyr Leu Gly Leu Ser Asp Tyr Phe Phe Asn Thr
110 250                     255                  260                  265
112 gcc ggg ctt gta tac caa gag gct ggg gtc ttg aag atg acc ctt aga     966
113 Ala Gly Leu Val Tyr Gln Glu Ala Gly Val Leu Lys Met Thr Leu Arg
114                270                     275                  280
116 gat gac atg att cca aag gag tcc aaa ttt cga ctg aca acc aag ttc     1014
117 Asp Asp Met Ile Pro Lys Glu Ser Lys Phe Arg Leu Thr Thr Lys Phe
118         285                     290                  295
120 ttt gga acc ttc cta cct gag gtg gcc aag aag ttt ccc aac atg aag     1062
121 Phe Gly Thr Phe Leu Pro Glu Val Ala Lys Lys Phe Pro Asn Met Lys
122         300                     305                  310
124 ata cag atc cat gtc tca gcc tcc acc ccg cca cac ctg tct gtg cag     1110
125 Ile Gln Ile His Val Ser Ala Ser Thr Pro Pro His Leu Ser Val Gln
126     315                     320                  325
128 ccc acc ggc ctt acc ttc tac cct gcc gtg gat gtc cag gcc ttt gcc     1158
129 Pro Thr Gly Leu Thr Phe Tyr Pro Ala Val Asp Val Gln Ala Phe Ala
130 330                     335                  340                  345
132 gtc ctc ccc aac tcc tcc ctg gct tcc ctc ttc ctg att ggc atg cac     1206
133 Val Leu Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile Gly Met His
134                350                     355                  360
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Input Set : C:\Crf3\Datahold\09543955
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```
136 aca act ggt tcc atg gag gtc agc gcc gag tcc aac agg ctt gtt gga  1254
137 Thr Thr Gly Ser Met Glu Val Ser Ala Glu Ser Asn Arg Leu Val Gly
138         365             370             375
140 gag ctc aag ctg gat agg ctg ctc ctg gaa ctg aag cac tca aat att  1302
141 Glu Leu Lys Leu Asp Arg Leu Leu Leu Glu Leu Lys His Ser Asn Ile
142         380             385             390
144 ggc ccc ttc ccg gtt gaa ttg ctg cag gat atc atg aac tac att gta  1350
145 Gly Pro Phe Pro Val Glu Leu Leu Gln Asp Ile Met Asn Tyr Ile Val
146         395             400             405
148 ccc att ctt gtg ctg ccc agg gtt aac gag aaa cta cag aaa ggc ttc  1398
149 Pro Ile Leu Val Leu Pro Arg Val Asn Glu Lys Leu Gln Lys Gly Phe
150 410             415             420             425
152 cct ctc ccg acg ccg gcc aga gtc cag ctc tac aac gta gtg ctt cag  1446
153 Pro Leu Pro Thr Pro Ala Arg Val Gln Leu Tyr Asn Val Val Leu Gln
154             430             435             440
156 cct cac cag aac ttc ctg ctg ttc ggt gca gac gtt gtc tat aaa      1491
157 Pro His Gln Asn Phe Leu Leu Phe Gly Ala Asp Val Val Tyr Lys
158             445             450             455
160 tgaaggcacc aggggtgccg ggggctgtca gccgcacctg ttcctgatgg gctgtggggc 1551
162 accggctgcc tttccccagg gaatcctctc cagatcttaa ccaagagccc cttgcaaact 1611
164 tcttcgactc agattcagaa atgatctaaa cacgaggaaa cattattcat tggaaaagtg 1671
166 catggtgtgt attttaggga ttatgagctt ctttcaaggg ctaaggctgc agagatattt 1731
168 cctccaggaa tcgtgtttca attgtaacca agaaatttcc atttgtgctt catgaaaaaa 1791
170 aacttctggt tttttttcatg tg                                        1813
173 <210> SEQ ID NO: 2
174 <211> LENGTH: 487
175 <212> TYPE: PRT
176 <213> ORGANISM: Homo sapiens
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179 Met Arg Glu Asn Met Ala Arg Gly Pro Cys Asn Ala Pro Arg Trp Val
180     -30             -25             -20
182 Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val
183 -15             -10             -5             -1   1
185 Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala
186             5               10              15
188 Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys
189         20              25              30
191 Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly
192     35              40              45
194 His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser
195 50              55              60              65
197 Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser
198             70              75              80
200 Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe
201         85              90              95
203 Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile
204         100             105             110
206 Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr
207     115             120             125
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```
209 Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His
210 130               135               140               145
212 Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys
213               150               155               160
215 Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys
216               165               170               175
218 Val Thr Asn Ser Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu
219               180               185               190
221 Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu
222       195               200               205
224 Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys
225 210               215               220               225
227 Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro
228               230               235               240
230 Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly
231               245               250               255
233 Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala
234               260               265               270
236 Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser
237       275               280               285
239 Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val
240 290               295               300               305
242 Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser
243               310               315               320
245 Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro
246               325               330               335
248 Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala
249               340               345               350
251 Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser
252       355               360               365
254 Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu
255 370               375               380               385
257 Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu
258               390               395               400
260 Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val
261               405               410               415
263 Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val
264               420               425               430
266 Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe
267       435               440               445
269 Gly Ala Asp Val Val Tyr Lys
270 450               455
274 <210> SEQ ID NO: 3
275 <211> LENGTH: 10
276 <212> TYPE: PRT
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: Description of Artificial Sequence: artificial
281       peptide XMP.365
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Input Set : C:\Crf3\Datahold\09543955
Output Set: N:\CRF3\09182001\I940921.raw

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283 <220> FEATURE:
284 <221> NAME/KEY: SITE
285 <222> LOCATION: (1)..(10)
286 <223> OTHER INFORMATION: Positions 1-10 are D-amino acids
288 <220> FEATURE:
289 <223> OTHER INFORMATION: The C-Terminus is Amidated
291 <400> SEQUENCE: 3
292 Lys Trp Leu Ile Gln Leu Phe His Lys Lys
293   1           5               10
296 <210> SEQ ID NO: 4
297 <211> LENGTH: 12
298 <212> TYPE: PRT
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Description of Artificial Sequence: artificial
303       peptide XMP.391
305 <220> FEATURE:
306 <223> OTHER INFORMATION: The C-Terminus is Amidated
308 <400> SEQUENCE: 4
310 Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys
311   1           5               10
314 <210> SEQ ID NO: 5
315 <211> LENGTH: 10
316 <212> TYPE: PRT
317 <213> ORGANISM: Artificial Sequence
319 <220> FEATURE:
320 <223> OTHER INFORMATION: Description of Artificial Sequence: artificial
321       peptide XMP.416
323 <220> FEATURE:
324 <221> NAME/KEY: SITE
325 <222> LOCATION: (1)..(10)
326 <223> OTHER INFORMATION: Positions 1-10 are D-amino acids
328 <220> FEATURE:
329 <223> OTHER INFORMATION: The C-Terminus is Amidated
331 <220> FEATURE:
332 <223> OTHER INFORMATION: 8-amino-octanyl group; NH2-(CH2)7-CO at N-Terminus
334 <400> SEQUENCE: 5
335 Lys Trp Leu Ile Gln Leu Phe His Lys Lys
336   1           5               10
339 <210> SEQ ID NO: 6
340 <211> LENGTH: 12
341 <212> TYPE: PRT
342 <213> ORGANISM: Artificial Sequence
344 <220> FEATURE:
345 <223> OTHER INFORMATION: Description of Artificial Sequence: artificial
346       peptide XMP.445
348 <220> FEATURE:
349 <221> NAME/KEY: SITE
350 <222> LOCATION: (1)
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/940,921

DATE: 09/18/2001
TIME: 10:36:17

Input Set : C:\Crf3\Datahold\09543955
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L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6